RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/593,672
Source: IFW
Date Processed by STIC: 9/29/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 09/29/2006
PATENT APPLICATION: **US/10/593,672** TIME: 11:06:50

Input Set : **F:\11281-118-999 - seqlist (final).txt**
Output Set: **N:\CRF4\09292006\J593672.raw**

<110> APPLICANT: Neurotech Pharmaceuticals Co., Ltd.
Han, Pyung Lim
Lee, Kang-Woo
Yang, Sung-Don
Song, Jin-Sook
<120> TITLE OF INVENTION: TRANSGENIC MICE INDUCING ALZHEIMER'S DISEASE EXPRESSING MUTANT BETACTF99
<130> FILE REFERENCE: 11281-118-999
C--> **<140> CURRENT APPLICATION NUMBER: US/10/593,672**
<141> CURRENT FILING DATE: 2006-09-20
<150> PRIOR APPLICATION NUMBER: KR 10-2004-0022562
<151> PRIOR FILING DATE: 2004-04-01
<160> NUMBER OF SEQ ID NOS: 25
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<213> ORGANISM: Homo sapiens
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cgcgatgctg cccggtttgg cactgctcct gctggccgcc tggacggctc gggcgctgga 180
ggtacccact gatggtaatg ctggcctgct ggctgaaccc cagattgcca tgttctgtgg 240
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caaaacctgc attgatacca aggaaggcat cctgcagtat tgccaagaag tctaccctga 360
actgcagatc accaatgtgg tagaagccaa ccaaccagtg accatccaga actggtgcaa 420
gcggggccgc aagcagtgca agacccatcc ccactttgtg attccctacc gctgcttagt 480
tggtgagttt gtaagtgatg cccttctcgt tcctgacaag tgcaaattct tacaccagga 540
gaggatggat gtttgcgaaa ctcatcttca ctggcacacc gtcgccaaag agacatgcag 600
tgagaagagt accaacttgc atgactacgg catgttgctg ccctgcggaa ttgacaagtt 660
ccgaggggta gagtttgtgt gttgcccact ggctgaagaa agtgacaatg tggattctgc 720
tgatgcggag gaggatgact cggatgtctg gtggggcgga gcagacacag actatgcaga 780
tgggagtgaa gacaaagtag tagaagtagc agaggaggaa gaagtggctg aggtggaaga 840
agaagaagcc gatgatgacg aggacgatga ggatggtgat gaggtagagg aagaggctga 900
ggaaccctac gaagaagcca cagagagaac caccagcatt gccaccacca ccaccaccac 960
cacagagtct gtggaagagg tggttcgaga ggtgtgctct gaacaagccg agacggggcc 1020
gtgccgagca atgatctccc gctggtactt tgatgtgact gaagggaagt gtgccccatt 1080
cttttacggc ggatgtggcg gcaaccggaa caactttgac acagaagagt actgcatggc 1140
cgtgtgtggc agcgccattc ctacaacagc agccagtacc cctgatgccg ttgacaagta 1200
tctcgagaca cctggggatg agaatgaaca tgcccatttc cagaaagcca aagagaggct 1260
tgaggccaag caccgagaga gaatgtccca ggtcatgaga gaatgggaag aggcagaacg 1320
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55 ggccagagtg gaagccatgc tcaatgaccg ccgccgcctg gccctggaga actacatcac 1500
56 cgctctgcag gctgttcctc ctcggcctcg tcacgtgttc aatatgctaa agaagtatgt 1560
57 ccgcgcagaa cagaaggaca gacagcacac cctaaagcat ttcgagcatg tgcgcatggt 1620
58 ggatcccaag aaagccgctc agatccggtc ccaggttatg acacacctcc gtgtgattta 1680
59 tgagcgcatg aatcagtctc tctccctgct ctacaacgtg cctgcagtgg ccgaggagat 1740
60 tcaggatgaa gttgatgagc tgcttcagaa agagcaaaac tattcagatg acgtcttggc 1800
61 caacatgatt agtgaaccaa ggatcagtta cggaaacgat gctctcatgc catctttgac 1860
62 cgaaacgaaa accaccgtgg agctccttcc cgtgaatgga gagttcagcc tggacgatct 1920
63 ccagccgtgg cattcttttg gggctgactc tgtgccagcc aacacagaaa acgaagttga 1980
64 gcctgttgat gcccgccctg ctgccgaccg aggactgacc actcgaccag gttctgggtt 2040
65 gacaaatatc aagacggagg agatctctga agtgaagatg gatgcagaat tccgacatga 2100
66 ctcaggatat gaagttcatc atcaaaaatt ggtgttcttt gcagaagatg tgggttcaaa 2160
67 caaaggtgca atcattggac tcatggtggg cggtgttgtc atagcgacag tgatcgtcat 2220
68 caccttggtg atgctgaaga agaaacagta cacatccatt catcatggtg tggtggaggt 2280
69 tgacgccgct gtcaccccag aggagcgcca cctgtccaag atgcagcaga acggctacga 2340
70 aaatccaacc tacaagttct ttgagcagat gcagaactag acccccgcca cagcagcctc 2400
71 tgaagttgga cagcaaaacc attgcttcac tacccatcgg tgtccattta tagaataatg 2460
72 tgggaagaaa caaacccgtt ttatgattta ctcattatcg ccttttgaca gctgtgctgt 2520
73 aacacaagta gatgcctgaa cttgaattaa tccacacatc agtaatgtat tctatctctc 2580
74 tttacatttt ggtctctata ctacattatt aatgggtttt gtgtactgta aagaatttag 2640
75 ctgtatcaaa ctagtgcatg aatagattct ctcctgatta tttatcacat agccccttag 2700
76 ccagttgtat attattcttg tggtttgtga cccaattaag tcctacttta catatgcttt 2760
77 aagaatcgat gggggatgct tcatgtgaac gtgggagttc agctgcttct cttgcctaag 2820
78 tattcctttc ctgatcacta tgcattttaa agttaaacat ttttaagtat ttcagatgct 2880
79 ttagagagat tttttttcca tgactgcatt ttactgtaca gattgctgct tctgctatat 2940
80 ttgtgatata ggaattaaga ggatacacac gtttgtttct tcgtgcctgt tttatgtgca 3000
81 cacattaggc attgagactt caagcttttc tttttttgtc cacgtatctt tgggtctttg 3060
82 ataaagaaaa gaatccctgt tcattgtaag cacttttacg gggcgggtgg ggaggggtgc 3120
83 tctgctggtc ttcaattacc aagaattc                                    3148
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86 <211> LENGTH: 751
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
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93 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
94             20                  25                  30
95 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
96         35                  40                  45
97 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
98     50                  55                  60
99 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
100 65                  70                  75                  80
101 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
102                 85                  90                  95
103 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
104             100                 105                 110
105 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
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PATENT APPLICATION: US/10/593,672 TIME: 11:06:50

Input Set : F:\11281-118-999 - seqlist (final).txt
Output Set: N:\CRF4\09292006\J593672.raw

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107 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
108     130                 135                 140
109 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
110 145                 150                 155                 160
111 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
112                 165                 170                 175
113 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
114             180                 185                 190
115 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
116         195                 200                 205
117 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
118     210                 215                 220
119 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
120 225                 230                 235                 240
121 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
122                 245                 250                 255
123 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
124             260                 265                 270
125 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
126         275                 280                 285
127 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
128     290                 295                 300
129 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
130 305                 310                 315                 320
131 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
132                 325                 330                 335
133 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
134             340                 345                 350
135 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
136         355                 360                 365
137 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
138     370                 375                 380
139 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
140 385                 390                 395                 400
141 Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
142                 405                 410                 415
143 Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
144             420                 425                 430
145 Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
146         435                 440                 445
147 Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
148     450                 455                 460
149 Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
150 465                 470                 475                 480
151 Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
152                 485                 490                 495
153 Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
154             500                 505                 510
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Input Set : F:\11281-118-999 - seqlist (final).txt
Output Set: N:\CRF4\09292006\J593672.raw

```
155 Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
156         515                 520                 525
157 Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
158     530                 535                 540
159 Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
160 545                 550                 555                 560
161 Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
162                 565                 570                 575
163 Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
164             580                 585                 590
165 Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
166         595                 600                 605
167 Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
168     610                 615                 620
169 Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
170 625                 630                 635                 640
171 Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
172                 645                 650                 655
173 Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
174             660                 665                 670
175 Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
176         675                 680                 685
177 Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
178     690                 695                 700
179 Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
180 705                 710                 715                 720
181 Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
182                 725                 730                 735
183 Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
184             740                 745                 750
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188 <211> LENGTH: 2256
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: C-terminal fragment of APP bearing V717F mutation
195 <400> SEQUENCE: 3
196 atgctgcccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
197 cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
198 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180
199 acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240
200 cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300
201 ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt 360
202 gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg 420
203 atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag 480
204 aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga 540
205 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
206 gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg 660
207 agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
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PATENT APPLICATION: **US/10/593,672** TIME: 11:06:50

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Output Set: **N:\CRF4\09292006\J593672.raw**

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208 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
209 ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
210 gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900
211 cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960
212 tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020
213 tgtggcagcg ccattcctac aacagcagcc agtacccctg atgccgttga caagtatctc 1080
214 gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140
215 gccaagcacc gagagagaat gtcccaggtc atgagagaat gggaagaggc agaacgtcaa 1200
216 gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtg 1260
217 gaatctttgg aacaggaagc agccaacgag agacagcagc tggtggagac acacatggcc 1320
218 agagtggaag ccatgctcaa tgaccgccgc cgcctggccc tggagaacta catcaccgct 1380
219 ctgcaggctg ttcctcctcg gcctcgtcac gtgttcaata tgctaaagaa gtatgtccgc 1440
220 gcagaacaga aggacagaca gcacacccta aagcatttcg agcatgtgcg catggtggat 1500
221 cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag 1560
222 cgcatgaatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag 1620
223 gatgaagttg atgagctgct tcagaaagag caaaactatt cagatgacgt cttggccaac 1680
224 atgattagtg aaccaaggat cagttacgga aacgatgctc tcatgccatc tttgaccgaa 1740
225 acgaaaacca ccgtggagct ccttcccgtg aatggagagt tcagcctgga cgatctccag 1800
226 ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct 1860
227 gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccaggttc tgggttgaca 1920
228 aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980
229 ggatatgaag ttcatcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040
230 ggtgcaatca ttggactcat ggtgggcggt gttgtcatag cgacagtgat cttcatcacc 2100
231 ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac 2160
232 gccgctgtca ccccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat 2220
233 ccaacctaca agttctttga gcagatgcag aactag                          2256
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 770
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 4
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243 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
244             20                  25                  30
245 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
246         35                  40                  45
247 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
248     50                  55                  60
249 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
250 65                  70                  75                  80
251 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
252                 85                  90                  95
253 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
254             100                 105                 110
255 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
256         115                 120                 125
257 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
258     130                 135                 140
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VERIFICATION SUMMARY DATE: 09/29/2006
PATENT APPLICATION: **US/10/593,672** TIME: 11:06:51

Input Set : **F:\11281-118-999 - seqlist (final).txt**
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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number